

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/765,120
Source: IFwo
Date Processed by STIC: 9/1/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

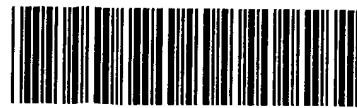
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/965,120</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <input type="checkbox"/> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004
TIME: 12:45:36

Input Set : A:\pto.lm.txt
Output Set: N:\CRF4\09012004\J765120.raw

1 <110> APPLICANT: Benner, Steven Albert
W--> 2 <120> TITLE OF INVENTION: Evolution-Based Functional Genomics
W--> 3 <140> CURRENT APPLICATION NUMBER: 10/765,120
W--> 0 <130> FILE REFERENCE:
4 <141> CURRENT FILING DATE: 2004-01-28
W--> 5 <160> NUMBER OF SEQ ID: 38
6 <170> SOFTWARE: MacIntosh OS 10.3 Microsoft Word v. 2003

ERRORED SEQUENCES

938 <210> SEQ ID NO: 14 486 shown (p.2)
939 <211> LENGTH: 478
940 <212> TYPE: PRT
941 <213> ORGANISM: Oryctolagus cuniculus
W--> 942 <400> SEQUENCE: 14
943 Met Leu Leu Glu Val Leu Asn Pro Arg His Tyr Asn Val Thr Ser
E--> 944 005 5 010 10 025 15 ← misaligned
945 Met Val Ser Glu Val Val Pro Ile Ala Ser Ile Ala Ile Leu Leu
946 020 025 030
947 Leu Thr Gly Phe Leu Leu Leu Val Trp Asn Tyr Glu Asp Thr Ser
948 035 040 045
949 Ser Ile Pro Gly Pro Ser Tyr Phe Leu Gly Ile Gly Pro Leu Ile
950 050 055 060
951 Ser His Cys Arg Phe Leu Trp Met Gly Ile Gly Ser Ala Cys Asn
952 065 070 075
953 Tyr Tyr Asn Lys Met Tyr Gly Glu Phe Met Arg Val Trp Val Cys
954 080 085 090
955 Gly Glu Glu Thr Leu Ile Ile Ser Lys Ser Ser Ser Met Phe His
956 095 100 105
957 Val Met Lys His Ser His Tyr Ile Ser Arg Phe Gly Ser Lys Leu
958 110 115 120
959 Gly Leu Gln Phe Ile Gly Met His Glu Lys Gly Ile Ile Phe Asn
960 125 130 135
961 Asn Asn Pro Ala Leu Trp Lys Ala Val Arg Pro Phe Phe Thr Lys
962 140 145 150
963 Ala Leu Ser Gly Pro Gly Leu Val Arg Met Val Thr Ile Cys Ala
964 155 160 165
965 Asp Ser Ile Thr Lys His Leu Asp Arg Leu Glu Glu Val Cys Asn
966 170 175 180
967 Asp Leu Gly Tyr Val Asp Val Leu Thr Leu Met Arg Arg Ile Met
968 185 190 195
969 Leu Asp Thr Ser Asn Met Leu Phe Leu Gly Ile Pro Leu Asp Glu

100% Not Comply
Corrected Diskette Needed

← misaligned
amino acid
numbers
(see item 3
on Error
Summary
sheet)

Please delete
0's (zeros)
before two-digit
amino acid numbers.
(see sample
Sequence Listing
attached in back,
for example)

also, see 1-822 of
Sequence Rules

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004
TIME: 12:45:36

Input Set : A:\pto.lm.txt
Output Set: N:\CRF4\09012004\J765120.raw

970	200	205	210
971	Ser Ala Ile Val Val Asn Ile Gln Gly	Tyr Phe Asp Ala Trp	Gln
972	215	220	225
973	Ala Leu Leu Leu Lys Pro Asp Ile Phe	Phe Lys Ile Ser Trp	Leu
974	230	235	240
975	Cys Arg Lys Tyr Glu Lys Ser Val Lys	Asp Leu Lys Asp Ala	Met
976	245	250	255
977	Glu Ile Leu Ile Ala Glu Lys Arg His	Arg Ile Ser Thr Ala	Glu
978	260	265	270
979	Lys Leu Glu Asp Ser Ile Asp Phe Ala	Thr Glu Leu Ile Phe	Ala
980	275	280	285
981	Glu Lys Arg Gly Glu Leu Thr Arg Glu	Asn Val Asn Gln Cys	Ile
982	290	295	300
983	Leu Glu Met Leu Ile Ala Ala Pro Asp	Thr Met Ser Val Ser	Val
984	305	310	315
985	Phe Phe Met Leu Phe Leu Ile Ala Lys	His Pro Gln Val Glu	Glu
986	320	325	330
987	Ala Ile Ile Arg Glu Ile Gln Thr Val	Val Gly Glu Arg Asp	Ile
988	335	340	345
989	Arg Ile Asp Asp Met Gln Lys Leu Lys	Val Val Glu Asn Phe	Ile
990	350	355	360
991	Asn Glu Ser Met Arg Tyr Gln Pro Val	Val Asp Leu Val Met	Arg
992	365	370	375
993	Lys Ala Leu Glu Asp Asp Val Ile Asp	Gly Tyr Pro Val Lys	Lys
994	380	385	390
995	Gly Thr Asn Ile Ile Leu Asn Leu Gly	Arg Met His Arg Leu	Glu
996	395	400	405
997	Phe Phe Pro Lys Pro Asn Glu Phe Thr	Leu Glu Asn Phe Ala	Lys
998	410	415	420
999	Asn Val Pro Tyr Arg Tyr Phe Gln Pro	Phe Gly Phe Gly Pro	Arg
1000	425	430	435
1001	Gly Cys Ala Gly Lys Tyr Ile Ala Met	Val Met Met Lys Val	Val
1002	440	445	450
1003	Leu Val Thr Leu Leu Arg Arg Phe His	Val Gln Thr Leu Gln	Gly
1004	455	460	465
1005	Arg Cys Val Glu Lys Met Gln Lys Lys	Asn Asp Leu Ser Leu	His
1006	470	475	480
1007	Pro Asp Glu Thr Arg Asp	←	
E--> 1008	485		
1151	<210> SEQ ID NO: 17		
1152	<211> LENGTH: 486		
1153	<212> TYPE: PRT		
1154	<213> ORGANISM: Poephila guttata		
W--> 1155	<400> SEQUENCE: 17		
1156	Met Phe Leu Glu Met Leu Asn Pro Met	His Tyr Asn Val Thr	Ile
1157	005	010	015
1158	Met Val Pro Glu Thr Val Pro Val Ser	Ala Met Pro Leu Leu	Leu
1159	020	025	030
1160	Ile Met Gly Leu Leu Leu Ile Arg Asn	Cys Glu Ser Ser	Ser

all P.3, 200

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:36

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

1161	835	840	845
1162	Ser Ile Pro Gly Pro Gly Tyr Cys Leu Gly Ile Gly Pro Leu Ile		
1163	850	855	860
1164	Ser His Gly Arg Phe Leu Trp Met Gly Ile Gly Ser Ala Cys Asn		
1165	865	870	875
1166	Tyr Tyr Asn Lys Met Tyr Gly Glu Phe Met Arg Val Trp Ile Ser		
1167	880	885	890
1168	Gly Glu Glu Thr Leu Ile Ile Ser Lys Ser Ser Ser Met Val His		
1169	895	100	105
1170	Val Met Lys His Ser Asn Tyr Ile Ser Arg Phe Gly Ser Lys Arg		
1171	110	115	120
1172	Gly Leu Gln Cys Ile Gly Met His Glu Asn Gly Ile Ile Phe Asn		
1173	125	130	135
1174	Asn Asn Pro Ser Leu Trp Arg Thr Val Arg Pro Phe Phe Met Lys		
1175	140	145	150
1176	Ala Leu Thr Gly Pro Gly Leu Ile Arg Met Val Glu Val Cys Val		
1177	155	160	165
1178	Glu Ser Ile Lys Gln His Leu Asp Arg Leu Gly Asp Val Thr Asp		
1179	170	175	180
1180	Asn Ser Gly Tyr Val Asp Val Val Thr Leu Met Arg His Ile Met		
1181	185	190	195
1182	Leu Asp Thr Ser Asn Thr Leu Phe Leu Gly Ile Pro Leu Asp Glu		
E--> 1183	200 200	205 205	210 210
E--> 1184	Ser Ser Ile Val Lys Lys Ile Gln Gly Tyr Phe Asn Ala Trp Gln		
E--> 1185	215	220	225
E--> 1186	Ala Leu Leu Ile Lys Pro Asn Ile Phe Phe Lys Ile Ser Trp Leu		
E--> 1187	230	235	240
E--> 1188	Tyr Arg Lys Tyr Glu Arg Ser Val Lys Asp Leu Lys Asp Glu Ile		
E--> 1189	245	250	255
E--> 1190	Glu Ile Leu Val Glu Lys Lys Arg Gln Lys Val Ser Ser Ala Glu		
E--> 1191	260	265	270
E--> 1192	Lys Leu Glu Asp Cys Met Asp Phe Ala Thr Asp Leu Ile Phe Ala		
E--> 1193	275	280	285
E--> 1194	Glu Arg Arg Gly Asp Leu Thr Lys Glu Asn Val Asn Gln Cys Ile		
E--> 1195	290	295	300
E--> 1196	Leu Glu Met Leu Ile Ala Ala Pro Asp Thr Met Ser Val Thr Leu		
E--> 1197	305	310	315
E--> 1198	Tyr Val Met Leu Leu Ile Ala Glu Tyr Pro Glu Val Glu Thr		
E--> 1199	320	325	330
E--> 1200	Ala Ile Leu Lys Glu Ile His Thr Val Val Gly Asp Arg Asp Ile		
E--> 1201	335	340	345
E--> 1202	Arg Ile Gly Asp Val Gln Asn Leu Lys Val Val Glu Asn Phe Ile		
E--> 1203	350	355	360
E--> 1204	Asn Glu Ser Leu Arg Tyr Gln Pro Val Val Asp Leu Val Met Arg		
E--> 1205	365	370	375
E--> 1206	Arg Ala Leu Glu Asp Asp Val Ile Asp Gly Tyr Pro Val Lys Lys		
E--> 1207	380	385	390
E--> 1208	Gly Thr Asn Ile Ile Leu Asn Ile Gly Arg Met His Arg Leu Glu		
E--> 1209	395	400	405

← misaligned
 amino acid
 numbers

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004
TIME: 12:45:36

Input Set : A:\pto.lm.txt
Output Set: N:\CRF4\09012004\J765120.raw

1210 Tyr Phe Pro Lys Pro Asn Glu Phe Thr Leu Glu Asn Phe Glu Lys
E--> 1211 410 415 420
 1212 Asn Val Pro Tyr Arg Tyr Phe Gln Pro Phe Gly Phe Gly Pro Arg
E--> 1213 425 430 435
 1214 Ser Cys Ala Gly Lys Tyr Ile Ala Met Val Met Met Lys Val Val
E--> 1215 440 445 450
 1216 Leu Val Thr Leu Leu Lys Arg Phe His Val Lys Thr Leu Gln Lys
E--> 1217 455 460 465
 1218 Arg Cys Ile Glu Asn Met Pro Lys Asn Asn Asp Leu Ser Leu His
E--> 1219 470 475 480
 1220 Leu Asp Glu Asp Ser Pro
E--> 1221 485
 1445 <210> SEQ ID NO: 35
 1446 <211> LENGTH: 83 84
 1447 <212> TYPE: DNA
 1448 <213> ORGANISM: Sus scrofa
W--> 1449 <400> SEQUENCE: 35
C--> 1450 caatcattac acgtgccat ttggcagcaa acttgggttg gaatcattg gcatgcata 60
E--> 1451 aaaaggcatca tgtttaacaa taa → group of 11
 1453 <210> SEQ ID NO: 36
 1454 <211> LENGTH: 84
 1455 <212> TYPE: DNA
 1456 <213> ORGANISM: Sus scrofa
W--> 1457 <400> SEQUENCE: 36
C--> 1458 tagtcactac acatcccgat ttggcagcaa acctgggttg cagttcattg gcatgcata 60
E--> 1459 gaaaggcatt atattcaaca ataa
 1461 <210> SEQ ID NO: 37
 1462 <211> LENGTH: 84
 1463 <212> TYPE: DNA
 1464 <213> ORGANISM: Sus scrofa
W--> 1465 <400> SEQUENCE: 37
C--> 1466 cagtcactac acatcccgat tcggcagcaa acctgggttg gagtgcatcg gcatgtatga 60
E--> 1467 gaagggcattc atatttaata atga
E--> 1469 <210> SEQ ID NO: 37 38 → change to
 1470 <211> LENGTH: 84
 1471 <212> TYPE: DNA
 1472 <213> ORGANISM: White lipped peccary
W--> 1473 <400> SEQUENCE: 37 38 → change to
C--> 1474 cagtcactac acatcccgat tcggcagcaa acctgggttg cagttcattg gaatgcata 60
E--> 1475 gaaaggcattc atatttaaca acaa

IMPORTANT: use lower-case letters
for nucleotides

84 ← insert
cumulative
base total
at right
margin
of each
line

84
↑
insert

84 ← insert

84 ← insert

10/765,120 5

<210> 26

<211> 50

<212> PRT

<213> Ancestral sequence

<400> 26

Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp
005 .010 .015

Leu Leu His Leu Leu Ala Ser Ser Lys Ser Cys Pro Leu Pro Gln
020 .025 030

Ala Arg Gly Leu Glu Thr Leu Glu Ser Leu Gly Gly Val Leu Glu
035 .040 .045

Ala Ser Leu Tyr Ser
050

invalid <213> response. See item 10 on
Euro Summary

Sheet.

Please
consult

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001
<141> 1998-12-31

<150> US 08/999,999
<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1
<211> 389
<212> DNA
<213> Paramecium sp.

<220>
<221> CDS
<222> (279)...(389)

<300>
<301> Doe, Richard
<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.
<303> Journal of Genes
<304> 1
<305> 4
<306> 1-7
<307> 1988-06-31
<308> 123456
<309> 1988-06-31

<400> 1
agctgttagtc attcctgtgt cctttctct ctgggcttct caccctgcta atcagatctc 60
agggagagtg tcttgaccct cctctgcctt tgcagcttca caggcaggca ggcaggcagc 120
tcatgtggca attgctggca gtgccacagg ctttcagcc aggcttaggg tgggttccgc 180
cgccggcgccg cggccccctct cgcgcctctc tcgcgcctct ctctcgctc cctctcgctc 240

ggacctgatt aggtgagcag gaggagggg cagttgc atg gtt tca atg ttc agc 296
Met Val Ser Met Phe 5 Ser Ser Ser Phe Ser Ser Ser Ser Ser Ser

tgc tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgt ttg ttc caa 344
Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val Cys Leu Phe Gln

tgt ccc aaa gtc ctc ccc tgt cac tca tca ctg cag ccg aat ctt 389
Cys Pro Lys Val Leu Pro Cys His Ser Ser Leu Gln Pro Asn Leu

<210> 2
<211> 37
<212> PRT
<213> Paramecium sp.

<400> 2
Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu 15
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100

Phe Val Cys Leu Phe Gln Cys Pro Lys Val Leu Pro Cys His Ser Ser

Leu Gln Pro Asn Leu
35

<210> 3
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3
Met Val Asn Leu Glu Pro Met His Thr Glu Ile 10
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100

<210> 4
<400> 4
000

[Annex VIII follows]

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:37

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

L:2 M:283 W: Missing Blank Line separator, <120> field identifier
L:3 M:283 W: Missing Blank Line separator, <140> field identifier
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:5 M:283 W: Missing Blank Line separator, <160> field identifier
L:12 M:283 W: Missing Blank Line separator, <400> field identifier
L:84 M:283 W: Missing Blank Line separator, <400> field identifier
L:156 M:283 W: Missing Blank Line separator, <400> field identifier
L:228 M:283 W: Missing Blank Line separator, <400> field identifier
L:300 M:283 W: Missing Blank Line separator, <400> field identifier
L:371 M:283 W: Missing Blank Line separator, <400> field identifier
L:443 M:283 W: Missing Blank Line separator, <400> field identifier
L:515 M:283 W: Missing Blank Line separator, <400> field identifier
L:585 M:283 W: Missing Blank Line separator, <400> field identifier
L:656 M:283 W: Missing Blank Line separator, <400> field identifier
L:728 M:283 W: Missing Blank Line separator, <400> field identifier
L:800 M:283 W: Missing Blank Line separator, <400> field identifier
L:872 M:283 W: Missing Blank Line separator, <400> field identifier
L:942 M:283 W: Missing Blank Line separator, <400> field identifier
L:944 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:1008 M:252 E: No. of Seq. differs, <211> LENGTH:Input:478 Found:486 SEQ:14
L:1014 M:283 W: Missing Blank Line separator, <400> field identifier
L:1086 M:283 W: Missing Blank Line separator, <400> field identifier
L:1155 M:283 W: Missing Blank Line separator, <400> field identifier
L:1183 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1185 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1187 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1189 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1191 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1193 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1195 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1197 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1199 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1201 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1203 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1205 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1207 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1209 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1211 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1213 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1215 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1217 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1219 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1221 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1227 M:283 W: Missing Blank Line separator, <400> field identifier
L:1241 M:283 W: Missing Blank Line separator, <400> field identifier
L:1255 M:283 W: Missing Blank Line separator, <400> field identifier
L:1269 M:283 W: Missing Blank Line separator, <400> field identifier
L:1283 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004
TIME: 12:45:37

Input Set : A:\pto.lm.txt
Output Set: N:\CRF4\09012004\J765120.raw

L:1297 M:283 W: Missing Blank Line separator, <400> field identifier
L:1311 M:283 W: Missing Blank Line separator, <400> field identifier
L:1325 M:283 W: Missing Blank Line separator, <400> field identifier
L:1339 M:283 W: Missing Blank Line separator, <400> field identifier
L:1353 M:283 W: Missing Blank Line separator, <400> field identifier
L:1367 M:283 W: Missing Blank Line separator, <400> field identifier
L:1381 M:283 W: Missing Blank Line separator, <400> field identifier
L:1395 M:283 W: Missing Blank Line separator, <400> field identifier
L:1409 M:283 W: Missing Blank Line separator, <400> field identifier
L:1419 M:283 W: Missing Blank Line separator, <400> field identifier
L:1429 M:283 W: Missing Blank Line separator, <400> field identifier
L:1439 M:283 W: Missing Blank Line separator, <400> field identifier
L:1449 M:283 W: Missing Blank Line separator, <400> field identifier
L:1450 M:112 C: (48) String data converted to lower case,
L:1451 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:35
L:1451 M:112 C: (48) String data converted to lower case,
L:1451 M:252 E: No. of Seq. differs, <211> LENGTH:Input:83 Found:84 SEQ:35
L:1457 M:283 W: Missing Blank Line separator, <400> field identifier
L:1458 M:112 C: (48) String data converted to lower case,
L:1459 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:36
L:1459 M:112 C: (48) String data converted to lower case,
L:1465 M:283 W: Missing Blank Line separator, <400> field identifier
L:1466 M:112 C: (48) String data converted to lower case,
L:1467 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:37
L:1467 M:112 C: (48) String data converted to lower case,
L:1469 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:37
L:1473 M:283 W: Missing Blank Line separator, <400> field identifier
L:1474 M:112 C: (48) String data converted to lower case,
L:1475 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:37
L:1475 M:112 C: (48) String data converted to lower case,